In accordance with 37 C.F.R. § 1.121, Applicants have provided (1) accurate instructions to amend the claims, (2) replacement claims in clean form herein, and (3) another version of the amended claims marked up to show all the changes relative to the previous version, which appears on an attached page.

I. Election/Restriction

In the Communication dated September 30, 2002, the Examiner has issued a restriction requirement in which the Examiner alleges that the claims of the application fall within two Groups of inventions as follows:

Group I: claims 1-20, 22, and 46, drawn to a peptide and a method of making the peptide; and

Group II: claims 23-44, drawn to a nucleic acid encoding the peptide, chimeric genes and vectors comprising the nucleic acid, host organisms transformed with the nucleic acid, a method of transforming host organisms, and a method of cultivating transformed plants.

The Examiner appears to acknowledge that a peptide and the nucleic acid encoding a peptide represent a single inventive concept under PCT rule 13.1. In addition, the Examiner appears to believe that the technical feature linking Groups I and II is a peptide with at least 6 cysteines, separated from each other by at least one amino acid. The Examiner then alleges that claim 1 is not novel in lieu of Hoffman et al. (1992, Immunol. Today, 13:411-415) because the Examiner contends that Hoffman et al. teach the sequence of several insect defensins that are peptides with at least 6 cysteines, separated from each other by at least one amino acid (Fig. 1) as claimed by the present invention. Because the Examiner concludes that claim 1, among others, is not novel, he contends that the technical feature linking Groups I and II is not special and therefore the groups should not be linked under PCT Rule 13.1.

The Examiner further contends that nucleotide sequences encoding different proteins are structurally distinct chemical compounds and are unrelated to one another, as are peptides with different amino acid sequences and states that such sequences constitute independent and distinct inventions within the meaning of 35 U.S.C. 121. The Examiner then states, absent evidence to the contrary, each such nucleotide or amino acid sequence is presumed to represent an independent and distinct invention, subject to restriction. Therefore, the Examiner has required that Applicants select a single nucleotide or amino acid sequence upon election of a Group, such requirement is said to not be an election of species.

Applicants respectfully disagree with the Examiner and hereby traverse the restriction requirement. First, Applicants point out that the Examiner has erroneously described the technical feature of Groups I and II as "a peptide with at least 6 cysteines, separated from each other by at least one amino acid." Claim 1 of the present application, as amended, is a genus claim which is directed to a peptide comprising the peptide sequence of Formula I

Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag (I)

in which:

Xaa is $-NH_2$ or a peptide residue consisting essentially of from 1 to 10 amino acids, preferably from 1 to 6 amino acids;

Xab is a peptide residue consisting essentially from 1 to 10 amino acids, preferably 10;

Xac is a peptide residue of 3 amino acids;

Xad is a peptide residue consisting essentially of from 1 to 9 amino acids, preferably 9;

Xae is a peptide residue consisting essentially of from 1 to 7 amino acids, preferably 7;

Xaf is a peptide residue of 1 amino acid; and

Xag is –OH or a peptide residue consisting essentially of from 1 to 5 amino acids, preferably 1 or 2 amino acids.

Claim 1, as amended, is written as a genus claim because the present invention has demonstrated that peptides that fall within this formula are heliomicine peptides – which is the crux of the present invention. The Examiner incorrectly describes the technical feature of claim 1, and others, as "a peptide with at least 6 cysteines, separated from each other by at least one amino acid." Claim 1 is directed to Formula I which has very specific requirements, including the inclusion of at least 6 cysteines. For example, Xab of Formula I is a peptide residue consisting essentially of from **1 to 10** amino acids; Xac is a peptide residue of **3 amino acids**, etc.

The Examiner then erroneously alleges that the peptides of Hoffman et al (Fig. 1) are peptides that fall within Formula I. Fig. 1 of Hoffman et al. shows 7 peptides. Peptides 1-6 of Fig. 1 do not fall within Formula I because the equivalent of Xab is more than 10 amino acids. Peptide 7 of Fig. 1 does not fall within Formula I because the equivalent of Xad is more than 9 amino acids. In fact, none of the peptides taught by Hoffman et al. fall within Formula I. Fig. 2 of Hoffman et al. depicts two additional peptides, of which the first peptide has more than 10 amino acids for the Xab equivalent; the second peptide has more than 3 amino acids for the Xac equivalent, more than 7 amino acids for the Xae equivalent and less than 1 amino acid for the Xaf equivalent. In addition, Fig. 4 of Hoffman et al. depicts four peptides, of which the first two peptides have more than 10 amino acids for the Xab equivalent; and the third and fourth peptides

have more than 9 amino acids for the Xad equivalent. Accordingly, none of the peptides of Hoffman et al. fall within the genus claimed in claim 1 of a peptide comprising the peptide sequence of Formula (I). Therefore, Applicants respectfully assert that claim 1, as amended, is novel and accordingly, the technical feature linking Group I and II is special and Groups I and II are properly linked under PCT Rule 13.1. Applicants therefore respectfully request that the restriction of the claims of the present invention into Group I and II be withdrawn and all the claims be examined in one application.

The Examiner has additionally contended that Applicants are required to select a single nucleotide or amino acid sequence for prosecution on the merits because these types of sequences, absent evidence to the contrary, are deemed to constitute independent and distinct inventions within the meaning of 35 USC 121. The Examiner states that nucleotide sequences encoding different proteins are structurally distinct "chemical compounds" and are unrelated to one another.

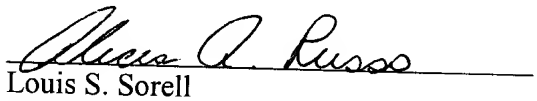
Applicants respectfully point out that it is proper to claim chemical compounds by a general formula when the invention relates to the characterization of the general formula, as in the present application. Applicants further wish to point out that under 37 CFR 1.141, cited by the Examiner, if an application includes an allowable generic claim (claim 1 of the present application), species claims may be examined in the same application as long as they are written in dependent form or otherwise include all the limitations of the generic claim. Applicants assert that all the claims of the present application include the limitations of generic claim 1 and therefore, as species claims of an allowable generic claim, may be examined together.

By requiring Applicants to choose a single nucleic acid or amino acid sequence to be examined in the present application, the Examiner is requiring a change in focus on the

disclosed invention. The invention is not directed to unrelated amino acid sequences or nucleic acid sequences encoding unrelated amino acid sequences, but rather is directed to heliomicine peptide amino acid as defined by Formula (I) and nucleic acids encoding a heliomicine peptide of Formula I. General Formula I, which defines the heliomicine peptides of the present invention, is the evidence to the contrary that shows that the sequences of the invention are not unrelated but rather fall within a genus, which supports Applicants traversal of the restriction requirement.

While Applicants believe that traversal of the restriction requirement is proper according to the remarks indicated above, should the Examiner find the remarks made herein unpersuasive, Applicants elect Group I and the heliomicine peptide as described by SEQ ID NO:2 for prosecution on the merits in the above-identified patent application in order to be fully responsive.

Respectfully submitted,



Louis S. Sorell
Patent Office Reg. No. 32,439

Alicia A. Russo
Patent Office Reg. No. 46,192

Attorneys for Applicants

BAKER BOTTS, L.L.P.
30 Rockefeller Plaza
New York, NY 10112
(212) 408-2500

## VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

1. (Amended) An isolated peptide comprising [essentially] the peptide sequence of formula (I),

Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag (I)

in which:

Xaa is $-NH_2$ or a peptide residue [comprising] consisting essentially of from 1 to 10 amino acids; preferably from 1 to 6 amino acids;

Xab is a peptide residue [comprising] consisting essentially of from 1 to 10 amino acids, preferably 10;

Xac is a peptide residue of 3 amino acids;

Xad is a peptide residue [comprising] consisting essentially of from 1 to 9 amino acids, preferably 9;

Xae is a peptide residue [comprising] consisting essentially of from 1 to 7 amino acids, preferably 7;

Xaf is a peptide residue of 1 amino acid; and

Xag is –OH or a peptide residue [comprising] consisting essentially of from 1 to 5 amino acids, preferably 1 or 2 amino acids.